

1. A method of creating a protein-binding profile of a test compound, comprising:
 - contacting the test compound with a library of nucleic acid/protein (NAP) conjugates, wherein each of said NAP conjugates comprises:
 - (a) a fusion protein comprising
 - (i) a nucleic acid modifying (NAM) enzyme, and
 - (ii) a candidate protein; and
 - (b) an expression vector comprising
 - (i) a fusion nucleic acid comprising a coding sequence for said NAM enzyme and a coding sequence for said candidate protein, and
 - (ii) an enzyme attachment sequence (EAS);wherein said EAS and said NAM enzyme are covalently linked, and wherein at least two of said NAP conjugates comprise different candidate proteins;
 - detecting the binding of said test compound to a NAP conjugate in the library;
 - and
 - identifying the candidate protein in the bound NAP conjugate by determining the nucleotide composition of the coding sequence for the candidate protein in said bound NAP conjugate,
 - thereby creating a protein-binding profile of said test compound comprising a list of candidate proteins to which said test compound binds.
2. The method of claim 1, wherein said NAM enzyme is a Rep protein.
3. The method of claim 1, wherein each of said NAP conjugates are produced by eukaryotic host cells containing the expression vectors.
4. The method of claim 1, wherein the coding sequence for the candidate protein is derived from a cDNA library.
5. The method of claim 1, further comprising the step of determining the binding affinity between the test compound and the bound NAP conjugate.
6. A method of determining the toxicity of a compound, comprising:
 - providing

(a) a first protein-binding profile of a first compound, said first compound being known to have a toxic effect in an animal species, and
(b) a second protein-binding profile of a second compound,
said first and second profiles each being obtained by a method of claim 1, wherein the coding sequence for the candidate protein is derived from said animal species; and
comparing said first and second profiles;
wherein substantial similarity between the two profiles is indicative of said second compound's having said toxic effect in said animal species.

7. A method of determining the toxicity of a compound, comprising:
providing

(a) a first protein-binding profile of said compound, said compound being known to have a toxic effect in a first animal species, and said first profile being obtained by a method of claim 1 in which the coding sequence for the candidate protein is derived from said first animal species; and

(b) a second protein-binding profile of said compound, said second profile being obtained by a method of claim 1 in which the coding sequence for the candidate protein is derived from a second animal species;

comparing said first and second profiles;
wherein substantial similarity between the two profiles is indicative of said compound's having said toxic effect in said second animal species.

8. A method of determining the toxicity of a compound, comprising:
providing

(a) a first protein-binding profile of said compound, said compound being known to have a toxic effect at a first organ of an animal species, and said first profile being obtained by a method of claim 1 in which the coding sequence for the candidate protein is derived from said first organ; and

(b) a second protein-binding profile of said compound, said second profile being obtained by a method of claim 1 in which the coding sequence for the candidate protein is derived from a second organ of said animal species;

comparing said first and second profiles;
wherein substantial similarity between the two profiles is indicative of said compound's having said toxic effect in said second organ.

9. A method of determining the toxicity of a compound, comprising:

providing

(a) a first protein-binding profile of said compound, said compound being known to have a toxic effect in an animal species at a first developmental stage, and said first profile being obtained by a method of claim 1 in which the coding sequence for the candidate protein is derived from said first animal species at said first developmental stage; and

(b) a second protein-binding profile of said compound, said second profile being obtained by a method of claim 1 in which the coding sequence for the candidate protein is derived from said animal species at a second developmental stage;

comparing said first and second profiles;

wherein substantial similarity between the two profiles is indicative of said compound's having said toxic effect in said second animal species at said second developmental stage.

10. A method of determining the toxicity of a compound, comprising:

providing a protein-binding profile of the compound, said profile being obtained by a method of claim 1,

determining whether the protein-binding profile includes one or more of the following: liver enzymes; cytochrome proteins; proteins encoded by multiple drug resistance genes; p450; and proteins associated with glutathione regulation, DNA repair, transcription regulation, structural maintenance, cell cycle control, and/or apoptosis; heat shock proteins; and housekeeping genes;

whereby such inclusion is indicative of said compound's having a toxic effect.